

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE

(iii) NUMBER OF SEQUENCES: 41

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/850,713
(B) FILING DATE: 02-MAY-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Becker, Cheryl L.
(B) REGISTRATION NUMBER: 35,441
(C) REFERENCE/DOCKET NUMBER: 6083.US.P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 847/935-1729
(B) TELEFAX: 847/938-2623
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGGCTGTAC	CAGGGCGTGC	CCAGAGCTGA	GCCGGGCACC	GAGGCCCGGA	GACACTATGA	60
TGAAGGCGTT	CGGATGGGCA	GCCTGGGGCT	GTTCCCTGCAG	TGCGCCATCT	CCCTGGTCTT	120
CTCTCTGGTC	ATGGACCGGC	TGGTGCAGCG	ATTCGGCACT	CGAGCAGTCT	ATTTGGCCAG	180
TGTGGCAGCT	TTCCCTGTGG	CTGCCGGTGC	CACATGCCTG	TCCCACAGTG	TGGCCGTGGT	240
GACAGCTTCA	GCCGCCTT					258

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCAGGGCGT	GCCCAGAGCT	GAGCCGGGCA	CCGAGGCCCG	GAGACACTAT	GATGAAGGCCG	60
TTCGGATGGG	CAGCCTGGGG	CTGTTCTGTC	AGTGCGCCAT	CTCCCTGGTC	TTCTCTCTGG	120
TCATGGACCG	GCTGGTGCAG	CGATTGCGCA	CTCGAGCAGT	CTATTTGGCC	AGTGTGGCAG	180
CTTTCCTGT	GGCTGCCGGT	GCCACATGCC	TGTCCCA			217

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 215
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACAGCTTCA	GCCGCCCTCA	CCGGGTTTCA	CTTCTCAGCC	CTGCAGATCC	TGCCCTACAC	60
ACTGGCCTCC	CTCTACCACC	GGGAGAAGCA	GGTGTTTCTG	CCCAAATACC	GAGGGGACAC	120
TGGAGGTGCT	AGCAGTGAGG	ACAGCCTGAT	GACCAGCTTC	CTGCCAGGCC	CTAAGCCTGG	180
AGCTCCCTTC	CCTAATGGAC	ACGTGGGTGC	TGGANGCAGT	GGCCTGCTCC	CACCTCCACC	240
CGCGCTCTGC	GGGGC					255

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTCCCTTCC	CTAATGGACA	CGTGGGTGCT	GGAGGCAGTG	GCCTGCTCCC	ACCTCCACCC	60
GCGCTCTGCG	GGGCCTCTGC	CTGTGATGTC	TCCGTACGTG	TGGTGGTGGG	TGAGCCCACC	120
GAGGCCAGGG	TGGTTCCGGG	CCGGGGCATC	TGCCTGGACC	TCGCCATCCT	GGATAGTGCC	180
TTCTGTCTGT	CCCAGGTGGC	CCCATCCCTG	TTTATGGGCT	CCATTGTCCA	GCTCAGCCAG	240
TCTGTCA						247

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGGATAGTGC	CTTCCTGCTG	TCCCAGGTGG	CCCCATCCCT	GTTTATGGGC	TCCATTGTCC	60
AGCTCAGCCA	GTCTGTCACT	GCCTATATGG	TGTCTGCCGC	AGGCTGGGTC	TGGTCGCCAT	120
TTACTTTGCT	ACACAGGTAG	TATTTGACAA	GAGCGACTTG	GCCAAATACT	CAGCGTAGAA	180
AACTTCCAGC	ACATTGGGGT	GGAGGGCCTG	CCTCACTGGG	TCCCAGCTCC	C	231

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 178
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTGGCCAAA	TACTCAGCGT	AGAAACTTC	CAGCACATTG	GGGTGGAGGG	CCTGCCTCAC	60
TGGGTCCCAG	CTCCCCGCTC	CTGTTAGCCC	CATGGGGCTG	CCGGGCTGGC	CGCCAGTTTC	120
TGTTGCTGCC	AAAGTAATGT	GGCTCTCTGC	TGCCACCCTG	TGCTGCTGAG	GTGCGTANTG	180
CACAGCTGGG	GGCTG					195

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 67
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 222
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCAGTTTCT	GTTGCTGCCA	AAGTAATGTG	GCTCTCTGCT	GCCACCCTGT	GCTGCTGAGG	60
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109240-4684860

TGCGTANTGC	ACAGCTGGGG	GCTGGGGCGT	CCCTCTCCTC	TCTCCCCAGT	CTCTAGGGCT	120
GCCTGACTGG	AGGCCTTCCA	AGGGGGTTTC	AGTCTGGACT	TATACAGGGA	GGCCAGAAGG	180
GCTCCATGCA	CTGGAATGCG	GGGACTCTGC	AGGTGGATTA	CNC		223

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 323
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCAGAAGGG	CTCCATGCAC	TGGAATGCGG	GGACTCTGCA	GGTGGATTAC	CCAGGCTCAG	60
GGTTAACAGC	TAGCCTCCTA	GTTGAGACAC	ACCTAGAGAA	GGGTTTTTGG	GAGCTGAATA	120
AACTCAGTCA	CCTGGTTTCC	CATCTCTAAG	CCCCTTAACC	TGCAGCTTCG	TTTAATGTAG	180
CTCTTGCAAT	GGAGTTTCTA	GGATGAAACA	CTCCTCCATG	GGATTTGAAC	ATATGAAAGT	240
TATTTGTAGG	GGAAGAGTCC	TGAGGGGCAA	CACACAAGAA	CCAGGTCCCC	TCAGCCCACA	300
GCAGTGTCTT	TTTGCTGATC	CANCCCCCTC	TTACTTTTAT	CA		342

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGAAGAGT	CCTGAGGGGC	AACACACAAG	AACCAGGTCC	CCTCAGCCCA	CAGCACTGTC	60
TTTTTGCTGA	TCCACCCCCC	TCTTACCTTT	TATCAGGATG	TGGCCTGTTG	GTCTTCTGT	120
TGCCATCACA	GAGACACAGG	CATTAAATA	TTTAACTTAT	TTATTTAACA	AAGTAGAAGG	180
GAATCCATTG	CTAGCTTTTC	TGTGTTGGTG	TCTAATATTT	GGGTAGGGTG	GGGGATCCCC	240
ACAATCAGG	TCCCCTGAGA	TAGCT				265

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 147
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCTTACCTT	TTATCAGGAT	GTGGCCTGTT	GGTCCTTCTG	TTGCCATCAC	AGAGACACAG	60
GCATTTAAAT	ATTTAACCTA	TTTATTTAAC	AAAGTAGAAG	GGAATCCATT	GCTAGCTTTT	120
CTGTGTTGGT	GTCTAATATT	TGGGTANGGT	GGGGGATCCC	CAACAATCAG	GTCCCCTGAG	180
ATAGCTGGTC	ATTGGGCTGA	TCATTGCCAG	AATCTTCTTC	TCCTGGGGTC	TGGCCCCCCA	240
AAATGCCTAA	CCCAGGACCT	TGGAAATTCT	ACTCATCCCA	AATGATAA		288

T03240-453430

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 216
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAATTCTACT	CATCCCAAAT	GATAATTCCA	AATGCTGTTA	CCCAAGGTTA	GGGTGTTGAA	60
GGAAGGTAGA	GGGTGGGGCT	TCAGGTCTCA	ACGGCTTCCC	TAACCACCCC	TCTTCTCTTG	120
GCCCAGCCTG	GTTCCCCCA	CTTCCACTCC	CCTCTACTCT	CTCTAGGACT	GGGCTGATGA	180
AGGCACTGCC	CAAAATTTCC	CCTACCCCCA	ACTTTNCCCT	ACCCCCAACT	TTCCCCACCA	240
GCTCCACAAC	CCTGTTTGA	GCTACTGCAG	GT			272

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 197
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAGGCACTGC	CCAAATNNC	CCCTACCCCC	AACTTTCCCC	TACCCCCAAC	TTTCCCCACC	60
AGCTCCACAA	CCCTGTTTGG	AGCTACTGCA	GGACCAGAAG	CACAAAGTGC	GGTTTCCCAA	120
GCCTTTGTCC	ATCTCAGCCC	CCAGAGTATA	TCTGTGCTTG	GGGAATCTCA	CACAGAAACT	180
CAGGAGCACC	CCCTGCNTGA	GCTAAGGGAG	GTCTTATCTC	TCAGGGGGGG	TTTAAGTGCC	240
GTTTGCAATA	ATGTCGTCTT	ATTTATTTAG	CGGGGTGAAT	ATTTTATACT	GTAA	294

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
(B) LOCATION: 113
(D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
(B) LOCATION: 147
(D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCCACAACC	CTGTTTGGAG	CTACTGCAGG	ACCAGAAGCA	CAAAGTGCGG	TTTCCCAAGC	60
CTTTGTCCAT	CTCAGCCCCC	AGAGTATATC	TGTGCTTGGG	GAATCTCACA	CANAAACTCA	120
GGAGCACCCC	CTGCCTGAGC	TAAGGGNGGT	C			151

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCAGAGTAT	ATCTGTGCTT	GGGGAATCTC	ACACAGAAAC	TCAGGAGCAC	CCCCTGCCTG	60
AGCTAAGGGA	GGTCTTATCT	CTCAGGGGGG	GTTTAAGTGC	CGTTTGCAAT	AATGTCGTCT	120
TATTTATTTA	GCGGGGTGAA	TATTTTATAC	TGTAAGTGAG	CAATCAGAGT	ATAATGTTTA	180
TGGTGACAAA	ATTAAAGGCT	TTCTTATATG	TTT			213

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACCAGGGCGT	GCCCAGAGCT	GAGCCGGGCA	CCGAGGCCCC	GAGACACTAT	GATGAAGGCG	60
TTCCGATGGG	CAGCCTGGGG	CTGTTCTGTC	AGTGCGCCAT	CTCCCTGGTC	TTCTCTCTGG	120
TCATGGACCG	GCTGGTGAG	CGATTGCGCA	CTCGAGCAGT	CTATTTGGCC	AGTGTGGCAG	180
CTTTCCCTGT	GGCTGCCGGT	GCCACATGCC	TGTCCACAG	TGTGGCCGTG	GTGACAGCTT	240
CAGCCGCCCT	CACCGGGTTC	ACCTTCTCAG	CCCTGCAGAT	CCTGCCCTAC	ACACTGGCCT	300
CCCTCTACCA	CCGGGAGAAG	CAGGTGTTCC	TGCCCCAATA	CCGAGGGGAC	ACTGGAGGTG	360
CTAGCAGTGA	GGACAGCCTG	ATGACCAGCT	TCCTGCCAGG	CCCTAAGCCT	GGAGCTCCCT	420
TCCCTAATGG	ACACGTGGGT	GCTGGAGGCA	GTGGCCTGCT	CCCACCTCCA	CCCGCGCTCT	480
GCGGGGCTTC	TGCCTGTGAT	GTCTCCGTAC	GTGTGGTGGT	GGGTGAGCCC	ACCGAGGCCA	540
GGGTGGTTCC	GGGCCGGGGC	ATCTGCCTGG	ACCTCGCCAT	CCTGGATAGT	GCCTTCCTGC	600
TGTCCAGGT	GGCCCCATCC	CTGTTTATGG	GCTCCATTGT	CCAGCTCAGC	CAGTCTGTCA	660
CTGCCTATAT	GGTGTCTGCC	GCAGGCCTGG	GTCTGGTTCG	CATTTACTTT	GCTACACAGG	720
TAGTATTTGA	CAAGAGCGAC	TTGGCCAAAT	ACTCAGCGTA	GAAAACCTCC	AGCACATTGG	780
GGTGGAGGGC	CTGCCTCACT	GGGTCCCAGC	TCCCCGCTCC	TGTTAGCCCC	ATGGGGCTGC	840
CGGGCTGGCC	GCCAGTTTCT	GTTGCTGCCA	AAGTAATGTG	GCTCTCTGCT	GCCACCCTGT	900
GCTGCTGAGG	TGCGTAGCTG	CACAGCTGGG	GGCTGGGGCG	TCCCTCTCCT	CTCTCCCCAG	960
TCTCTAGGGC	TGCCTGACTG	GAGGCCTTCC	AAGGGGGTTT	CAGTCTGGAC	TTATACAGGG	1020
AGGCCAGAAG	GGCTCCATGC	ACTGGAATGC	GGGACTCTGC	AGGTGGATTA	CCCAGGCTCA	1080
GGGTTAACAG	CTAGCCTCCT	AGTTGAGACA	CACCTAGAGA	AGGGTTTTTG	GGAGCTGAAT	1140
AAACTCAGTC	ACCTGGTTTC	CCATCTCTAA	GCCCCTTAAC	CTGCAGCTTC	GTTTAATGTA	1200
GCTCTTGCAI	GGGAGTTTCT	AGGATGAAAC	ACTCCTCCAT	GGGATTTGAA	CATATGAAAG	1260
TTATTTGTAG	GGGAAGAGTC	CTGAGGGGCA	ACACACAAGA	ACCAGGTCCC	CTCAGCCCAC	1320

AGCACTGTCT	TTTTGCTGAT	CCACCCCCCT	CTTACCTTTT	ATCAGGATGT	GGCCTGTTGG	1380
TCCTTCTGTT	GCCATCACAG	AGACACAGGC	ATTTAAATAT	TTAACTTATT	TATTTAACAA	1440
AGTAGAAGGG	AATCCATTGC	TAGCTTTTCT	GTGTTGGTGT	CTAATATTTG	GGTAGGGTGG	1500
GGGATCCCCA	ACAATCAGGT	CCCCTGAGAT	AGCTGGTCAT	TGGGCTGATC	ATTGCCAGAA	1560
TCTTCTTCTC	CTGGGGTCTG	GGCCCCCAAA	ATGCCTAACC	CAGGACCTTG	GAAATTCTAC	1620
TCATCCCCAA	TGATAATTCC	AAATGCTGTT	ACCCAAGGTT	AGGGTGTGTA	AGGAAGGTAG	1680
AGGGTGGGGC	TTCAGGTCTC	AACGGCTTCC	CTAACCACCC	CTCTTCTCTT	GGCCAGCCTT	1740
GGTTCCCCCC	ACTTCCACTC	CCCTCTACTC	TCTCTAGGAC	TGGGCTGATG	AAGGCAC'TGC	1800
CCAAAATTTT	CCCTACCCCC	AACTTTCCCC	TACCCCCAAC	TTTCCCCACC	AGCTCCACAA	1860
CCCTGTTTGG	AGCTACTGCA	GGACCAGAAG	CACAAAGTGC	GGTTTCCCCA	GCCTTTGTCC	1920
ATCTCAGCCC	CCAGAGTATA	TCTGTGCTTG	GGGAATCTCA	CACAGAAACT	CAGGAGCACC	1980
CCCTGCCTGA	GCTAAGGGAG	GTCTTATCTC	TCAGGGGGGG	TTTAAGTGCC	GTTTGCAATA	2040
ATGTCGTCTT	ATTTTTTTAG	CGGGGTGAAT	ATTTTATACT	GTAAGTGAGC	AATCAGAGTA	2100
TAATGTTTAT	GGTGACAAAA	TTAAAGGCTT	TCTTATATGT	TTA		2143

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGGGCTGTAC	CAGGGCGTGC	CCAGAGCTGA	GCCGGGCACC	GAGGCCCCGA	GACACTATGA	60
TGAAGGCGTT	CGGATGGGCA	GCCTGGGGCT	GTTCCCTGCAG	TGCGCCATCT	CCCTGGTCTT	120
CTCTCTGGTC	ATGGACCGGC	TGGTGCAGCG	ATTCGGCACT	CGAGCAGTCT	ATTTGGCCAG	180
TGTGGCAGCT	TTCCCTGTGG	CTGCCGGTGC	CACATGCCTG	TCCCACAGTG	TGGCCGTGGT	240
GACAGCTTCA	GCCGCCCTCA	CCGGGTTTCA	CTTCTCAGCC	CTGCAGATCC	TGCCCTACAC	300
ACTGGCCTCC	CTCTACCACC	GGGAGAAGCA	GGTGTTCCTG	CCCAAATACC	GAGGGGACAC	360
TGGAGGTGCT	AGCAGTGAGG	ACAGCCTGAT	GACCAGCTTC	CTGCCAGGCC	CTAAGCCTGG	420
AGCTCCCTTC	CCTAATGGAC	ACGTGGGTGC	TGGAGGCAGT	GGCCTGCTCC	CACCTCCACC	480
CGCGCTCTGC	GGGGCCTCTG	CCTGTGATGT	CTCCGTACGT	GTGGTGGTGG	GTGAGCCAC	540
CGAGGCCAGG	GTGGTTCCGG	GCCGGGGCAT	CTGCCTGGAC	CTCGCCATCC	TGGATAGTGC	600
CTTCCTGCTG	TCCCAGGTGG	CCCCATCCCT	GTTTATGGGC	TCCATTGTCC	AGCTCAGCCA	660
GTCTGTCACT	GCCTATATGG	TGTCTGCCGC	AGGCCTGGGT	CTGGTCGCCA	TTTACTTTGC	720
TACACAGGTA	GTATTTGACA	AGAGCGACTT	GGCCAAATAC	TCAGCGTAGA	AAACTTCCAG	780
CACATTGGGG	TGGAGGGCCT	GCCTCACTGG	GTCCCAGCTC	CCCCGCTCCTG	TTAGCCCCAT	840
GGGGCTGCCG	GCTGGGCCCG	CAGTTTCTGT	TGCTGCCAAA	GTAATGTGGC	TCTCTGCTGC	900
CACCCTGTGC	TGCTGAGGTG	CGTAGCTGCA	CAGCTGGGGG	CTGGGGCGTC	CCTCTCCTCT	960
CTCCCCAGTC	TCTAGGGCTG	CCTGACTGGA	GGCCTTCCAA	GGGGGTTTCA	GTCTGGACTT	1020
ATACAGGGAG	GCCAGAAGGG	CTCCATGCAC	TGGAATGCGG	GGACTCTGCA	GGTGGATTAC	1080
CCAGGCTCAG	GGTTAACAGC	TAGCCTCCTA	GTTGAGACAC	ACCTAGAGAA	GGGTTTTTGG	1140
GAGCTGAATA	AACTCAGTCA	CCTGGTTTCC	CATCTCTAAG	CCCCTTAACC	TGCAGCTTCG	1200
TTTAATGTAG	CTCTTGCAAT	GGAGTTTCTA	GGATGAAACA	CTCCTCCATG	GGATTTGAAC	1260
ATATGAAAGT	TATTTGTAGG	GGAAGAGTCC	TGAGGGGCAA	CACACAAGAA	CCAGGTCCCC	1320
TCAGCCCCA	GCCTGTCTTT	TTTGCTGATC	CACCCCCCTC	TTACCTTTTA	TCAGGATGTG	1380
GCCTGTTGGT	CCTTCTGTTG	CCATCACAGA	GACACAGGCA	TTTAAATATT	TAACTTATTT	1440
ATTTAACAAA	GTAGAAGGGA	ATCCATTGCT	AGCTTTTCTG	TGTTGGTGTG	TAATATTTTG	1500
GTAGGGTGGG	GGATCCCCAA	CAATCAGGTC	CCCTGAGATA	GCTGGTCATT	GGGCTGATCA	1560
TTGCCAGAAT	CTTCTTCTCC	TGGGGTCTGG	CCCCCAAAA	TGCCTAACCC	AGGACCTTGG	1620
AAATTCTACT	CATCCCAAAT	GATAATTCCA	AATGCTGTTA	CCCAAGGTTA	GGGTGTTGAA	1680
GGAGGCTAGA	GGGTGGGGCT	TCAGGTCTCA	ACGGCTTCCC	TAACCACCCC	TCTTCTCTTG	1740
GCCCAGCCTG	TTCCCCCCCA	CTTCACTCTC	CTCTACTCTT	CTCTAGGACT	GGGCTGATGA	1800
AGGCACTGCC	CAAAATTTCC	CCTACCCCCA	ACTTTCCCCCT	ACCCCCAACT	TTCCCCACCA	1860
GCTCCACAAC	CCTGTTTGGG	GCTACTGCAG	GACCAGAAGC	ACAAAGTGCG	GTTTCCCAAG	1920
CCTTTGTCCA	TCTCAGCCCC	CAGAGTATAT	CTGTGCTTGG	GGAATCTCAC	ACAGAAACTC	1980
AGGAGCAACC	CCTGCCCTGAG	CTAAGGGAGG	TCTTATCTCT	CAGGGGGGGT	TTAAGTGCCG	2040
TTTGCAATAA	TGTCGTCTTA	TTTATTTTAT	GGGGTGAATA	TTTTATACTG	TAAAGTGAGCA	2100
ATCAGAGTAT	AATGTTTATG	GTGACAAAAA	TAAAGGCTTT	CTTATATGTT	TA	2152

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC 60
CGGGAATT 68

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG 60
GAATTCGG 68

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCGGATAAC AATTTACAC AGGA 24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTAAAACGA CGGCCAGT 18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGTTCTGCC CAAATACC 18

(2) INFORMATION FOR SEQ ID NO:22:

TOCCTD-165TH860

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTCTGGTCG CCATTAC

18

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGGGCAACAC ACAAGAAC

18

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCAGCCCCCA GAGTATATC

19

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTCCATGCA CTGGAATG

18

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACCCAGGACC TTGGAAAT

18

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

TOP SECRET

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACACCCTAAC CTTGGGTAAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCTAGAAACT CCCATGCAAG

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TGGCAGCAAC AGAAACTG

18

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ACTATCCAGG ATGGCGAG

18

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGATTGCTCA CTTACAGT

18

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGTTAGGGA AGCCGTTG

18

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCCCAATGA CCAGCTAT

18

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTCCAAATGC TGTTACCCAA GG

22

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTGCTCCTG AGTTTCTGTG TGAG

24

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg
1				5					10					15	
Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser	Leu	Gly	Leu	Phe	Leu
			20				25						30		
Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val	Met	Asp	Arg	Leu	Val
		35				40						45			

Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala Ser Val Ala Ala Phe
50 55 60
Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His Ser Val Ala Val Val
65 70 75 80
Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile
85 90 95
Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe
100 105 110
Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser
115 120 125
Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro
130 135 140
Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro
145 150 155 160
Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser Val Arg Val Val Val
165 170 175
Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly Arg Gly Ile Cys Leu
180 185 190
Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro
195 200 205
Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala
210 215 220
Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala
225 230 235 240
Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
245 250 255

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr
1 5 10 15
Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly
20 25 30
Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val
35 40

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly Arg
1 5 10 15
Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser
20 25

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: None

Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg
1 5 10 15
Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
20 25

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

(2) INFORMATION FOR SEQ ID NO:41:

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/ SEQUENCE CHARACTERISTICS
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1 5 10 15
His His His His His
20